

H12



PCT

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/09/554,960**

**DATE: 06/30/2004**  
**TIME: 13:03:05**

**Input Set : A:\Nih342-1.app**  
**Output Set: N:\CRF4\06302004\I554960.raw**

3 <110> APPLICANT: Kaslow, David C.  
 4 Tsuboi, Takafumi  
 5 Torii, Motomi  
 6 The Government of the United States of America  
 7 as represented by the Secretary of the  
 8 Department of Health and Human Services  
 10 <120> TITLE OF INVENTION: Vaccines for Blocking Transmission of Plasmodium vivax  
 12 <130> FILE REFERENCE: 015280-34210US  
 14 <140> CURRENT APPLICATION NUMBER: US 09/554,960  
 C--> 15 <141> CURRENT FILING DATE: 2000-05-22  
 17 <150> PRIOR APPLICATION NUMBER: US 60/045,283  
 18 <151> PRIOR FILING DATE: 1997-05-01  
 20 <150> PRIOR APPLICATION NUMBER: WO PCT/US98/25742  
 21 <151> PRIOR FILING DATE: 1998-12-04  
 23 <160> NUMBER OF SEQ ID NOS: 24  
 25 <170> SOFTWARE: PatentIn Ver. 2.0  
 27 <210> SEQ ID NO: 1  
 28 <211> LENGTH: 1066  
 29 <212> TYPE: DNA  
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 34 <222> LOCATION: (147)..(857)  
 35 <223> OTHER INFORMATION: Pvs28  
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 42 acttttgcgc ctcccccttg ttcaaa atg aat acc tac cac agc ttg ctg ttc 173  
 43 Met Asn Thr Tyr His Ser Leu Leu Phe  
 44 1 5  
 46 ctt ctg gcc atc gtg ctt act gtt aag cac acc ttc gca aag gtc acc 221  
 47 Leu Leu Ala Ile Val Leu Thr Val Lys His Thr Phe Ala Lys Val Thr  
 48 10 15 20 25  
 50 gcg gag acc caa tgc aaa aat ggc tat gta gtc caa atg agc aat cat 269  
 51 Ala Glu Thr Gln Cys Lys Asn Gly Tyr Val Val Gln Met Ser Asn His  
 52 30 35 40  
 54 ttt gaa tgc aaa tgc aac gac ggg ttt gtt atg gca aat gaa aac act 317  
 55 Phe Glu Cys Lys Cys Asn Asp Gly Phe Val Met Ala Asn Glu Asn Thr  
 56 45 50 55  
 58 tgc gag gaa aaa cgc gat tgc aca aat cca caa aat gta aat aaa aac 365  
 59 Cys Glu Glu Lys Arg Asp Cys Thr Asn Pro Gln Asn Val Asn Lys Asn  
 60 60 65 70  
 62 tgt gga gac tac gct gtg tgt gca aac acc aga atg aat gat gag gaa 413

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63 Cys Gly Asp Tyr Ala Val Cys Ala Asn Thr Arg Met Asn Asp Glu Glu  
64 75 80 85  
66 aga gca tta cga tgc ggc tgc ata tta ggg tac acc gta atg aat gag 461  
67 Arg Ala Leu Arg Cys Gly Cys Ile Leu Gly Tyr Thr Val Met Asn Glu  
68 90 95 100 105  
70 gtg tgt act cca aat aaa tgt aac ggc gtt ttg tgt gga aag gga aag 509  
71 Val Cys Thr Pro Asn Lys Cys Asn Gly Val Leu Cys Gly Lys Gly Lys  
72 110 115 120  
74 tgc atc tta gat ccc gct aat gtg aac agc acc atg tgc tct tgt aat 557  
75 Cys Ile Leu Asp Pro Ala Asn Val Asn Ser Thr Met Cys Ser Cys Asn  
76 125 130 135  
78 ata gga acc aca ttg gat gaa tct aaa aaa tgt gga aag cca gga aaa 605  
79 Ile Gly Thr Thr Leu Asp Glu Ser Lys Lys Cys Gly Lys Pro Gly Lys  
80 140 145 150  
82 act gaa tgc acg ttg aag tgt aag gca aac gaa gaa tgt aaa gag act 653  
83 Thr Glu Cys Thr Leu Lys Cys Lys Ala Asn Glu Cys Lys Glu Thr  
84 155 160 165  
86 cag aat tat tac aag tgc gtt gcg aag gga agc ggc gga gaa ggc agc 701  
87 Gln Asn Tyr Tyr Lys Cys Val Ala Lys Gly Ser Gly Gly Glu Gly Ser  
88 170 175 180 185  
90 ggt gga gaa ggc agc ggc gga gag ggc agc ggc gga gag ggc agc ggc 749  
91 Gly Gly Glu Gly Ser Gly Glu Gly Ser Gly Gly Glu Gly Ser Gly  
92 190 195 200  
94 gga gag ggc agc ggt gga gac aca gga gca gct tac agt ctc atg aac 797  
95 Gly Glu Gly Ser Gly Gly Asp Thr Gly Ala Ala Tyr Ser Leu Met Asn  
96 205 210 215  
98 gga tct gca gta atc agc ata cta ctt gta ttc gcc ttc atg atg 845  
99 Gly Ser Ala Val Ile Ser Ile Leu Leu Val Phe Ala Phe Phe Met Met  
100 220 225 230  
102 tca tta gtg tagacgattc tacacacaca cacaacata cacaaggaaa 894  
103 Ser Leu Val  
104 235  
106 gaagcgtctc acagagtcat ttcaagtcat acgcacaaaa aaggaaagta catccagctg 954  
108 gtgaaagagc atttatgtgt gcagttatcc ttgggagaag caccctccac ccagttgcgt 1014  
110 tgctgttacc ttaaaactta gtggcaccca tatcgaattt gactttgctc gc 1066  
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122 Val Lys His Thr Phe Ala Lys Val Thr Ala Glu Thr Gln Cys Lys Asn  
123 20 25 30  
125 Gly Tyr Val Val Gln Met Ser Asn His Phe Glu Cys Lys Cys Asn Asp  
126 35 40 45  
128 Gly Phe Val Met Ala Asn Glu Asn Thr Cys Glu Glu Lys Arg Asp Cys  
129 50 55 60  
131 Thr Asn Pro Gln Asn Val Asn Lys Asn Cys Gly Asp Tyr Ala Val Cys

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Input Set : A:\Nih342-1.app  
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132	65	70	75	80
134	Ala Asn Thr Arg Met Asn Asp Glu Glu Arg Ala Leu Arg Cys Gly Cys			
135		85	90	95
137	Ile Leu Gly Tyr Thr Val Met Asn Glu Val Cys Thr Pro Asn Lys Cys			
138		100	105	110
140	Asn Gly Val Leu Cys Gly Lys Gly Lys Cys Ile Leu Asp Pro Ala Asn			
141		115	120	125
143	Val Asn Ser Thr Met Cys Ser Cys Asn Ile Gly Thr Thr Leu Asp Glu			
144		130	135	140
146	Ser Lys Lys Cys Gly Lys Pro Gly Lys Thr Glu Cys Thr Leu Lys Cys			
147		145	150	155
149	Lys Ala Asn Glu Glu Cys Lys Glu Thr Gln Asn Tyr Tyr Lys Cys Val			
150		165	170	175
152	Ala Lys Gly Ser Gly Gly Glu Gly Ser Gly Gly Glu Gly Ser Gly Gly			
153		180	185	190
155	Glu Gly Ser Gly Gly Glu Gly Ser Gly Gly Glu Gly Ser Gly Gly Asp			
156		195	200	205
158	Thr Gly Ala Ala Tyr Ser Leu Met Asn Gly Ser Ala Val Ile Ser Ile			
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161	Leu Leu Val Phe Ala Phe Phe Met Met Ser Leu Val			
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171	<221> NAME/KEY: CDS			
172	<222> LOCATION: (255)..(914)			
173	<223> OTHER INFORMATION: Pvs25			
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178	tttcgattgt ttgcttgtt gctttttgc ttattcgccc gttttccgc ttgcccggtc	120		
180	gccccgtcca caacgcgccc ctgcaaagt tgccaccac cgaccacaaa aaccttattca	180		
182	ccaccatccg agcggaaagg aacgcgcgccc actgtgctgc ctacctcccc gaataacaac	240		
184	tccacttagc caaa atg aac tcc tac tac agc ctc ttc gtt ttt ttc ctc	290		
185	Met Asn Ser Tyr Tyr Ser Leu Phe Val Phe Phe Leu			
186		1	5	10
188	gtc caa att gcg cta aag tat agc aag gca gcc gtc acg gta gac acc	338		
189	Val Gln Ile Ala Leu Lys Tyr Ser Lys Ala Ala Val Thr Val Asp Thr			
190		15	20	25
192	ata tgc aaa aat gga cag ctg gtt caa atg agt aac cac ttt aag tgt	386		
193	Ile Cys Lys Asn Gly Gln Leu Val Gln Met Ser Asn His Phe Lys Cys			
194		30	35	40
196	atg tgt aac gaa ggg ctg gtg cac ctt tcc gaa aat aca tgt gaa gaa	434		
197	Met Cys Asn Glu Gly Leu Val His Leu Ser Glu Asn Thr Cys Glu Glu			
198		45	50	55
200	aaa aat gaa tgc aag aaa gaa acc cta ggc aaa gca tgc ggg gaa ttt	482		
201	Lys Asn Glu Cys Lys Lys Glu Thr Leu Gly Lys Ala Cys Gly Glu Phe			
202		65	70	75

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204 ggc cag tgt ata gaa aac cca gac cca gca cag gta aac atg tac aaa 530  
 205 Gly Gln Cys Ile Glu Asn Pro Asp Pro Ala Gln Val Asn Met Tyr Lys  
 206 80 85 90  
 208 tgt ggt tgc att gag ggc tac act ttg aag gaa gac act tgt gtg ctt 578  
 209 Cys Gly Cys Ile Glu Gly Tyr Thr Leu Lys Glu Asp Thr Cys Val Leu  
 210 95 100 105  
 212 gat gta tgt caa tac aaa aat tgt gga gaa agt ggc gaa tgc att gtt 626  
 213 Asp Val Cys Gln Tyr Lys Asn Cys Gly Glu Ser Gly Glu Cys Ile Val  
 214 110 115 120  
 216 gag tac ctc tcg gaa atc caa agt gca ggt tgc tca tgt gct att ggc 674  
 217 Glu Tyr Leu Ser Glu Ile Gln Ser Ala Gly Cys Ser Cys Ala Ile Gly  
 218 125 130 135 140  
 220 aaa gtc ccc aat cca gaa gat gag aaa aaa tgt acc aaa acg gga gaa 722  
 221 Lys Val Pro Asn Pro Glu Asp Glu Lys Lys Cys Thr Lys Thr Gly Glu  
 222 145 150 155  
 224 act gct tgt caa ttg aaa tgt aac aca gat aat gaa gtc tgc aaa aat 770  
 225 Thr Ala Cys Gln Leu Lys Cys Asn Thr Asp Asn Glu Val Cys Lys Asn  
 226 160 165 170  
 228 gtt gaa gga gtt tac aag tgc cag tgt atg gaa ggc ttt acg ttc gac 818  
 229 Val Glu Gly Val Tyr Lys Cys Gln Cys Met Glu Gly Phe Thr Phe Asp  
 230 175 180 185  
 232 aaa gag aaa aat gta tgc ctt tcc tat tct gta ttt aac atc cta aac 866  
 233 Lys Glu Lys Asn Val Cys Leu Ser Tyr Ser Val Phe Asn Ile Leu Asn  
 234 190 195 200  
 236 tac tcc ctc ttc ttt atc atc ctg ctt gtc ctt tcg tac gtc ata 911  
 237 Tyr Ser Leu Phe Phe Ile Ile Leu Leu Val Leu Ser Tyr Val Ile  
 238 205 210 215  
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 247 <212> TYPE: PRT  
 248 <213> ORGANISM: Plasmodium vivax  
 250 <400> SEQUENCE: 4  
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 254 Leu Lys Tyr Ser Lys Ala Ala Val Thr Val Asp Thr Ile Cys Lys Asn  
 255 20 25 30  
 257 Gly Gln Leu Val Gln Met Ser Asn His Phe Lys Cys Met Cys Asn Glu  
 258 35 40 45  
 260 Gly Leu Val His Leu Ser Glu Asn Thr Cys Glu Glu Lys Asn Glu Cys  
 261 50 55 60  
 263 Lys Lys Glu Thr Leu Gly Lys Ala Cys Gly Glu Phe Gly Gln Cys Ile  
 264 65 70 75 80  
 266 Glu Asn Pro Asp Pro Ala Gln Val Asn Met Tyr Lys Cys Gly Cys Ile  
 267 85 90 95  
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 272 Tyr Lys Asn Cys Gly Glu Ser Gly Glu Cys Ile Val Glu Tyr Leu Ser

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273      115          120          125
275 Glu Ile Gln Ser Ala Gly Cys Ser Cys Ala Ile Gly Lys Val Pro Asn
276      130          135          140
278 Pro Glu Asp Glu Lys Lys Cys Thr Lys Thr Gly Glu Thr Ala Cys Gln
279      145          150          155          160
281 Leu Lys Cys Asn Thr Asp Asn Glu Val Cys Lys Asn Val Glu Gly Val
282          165          170          175
284 Tyr Lys Cys Gln Cys Met Glu Gly Phe Thr Phe Asp Lys Glu Lys Asn
285          180          185          190
287 Val Cys Leu Ser Tyr Ser Val Phe Asn Ile Leu Asn Tyr Ser Leu Phe
288          195          200          205
290 Phe Ile Ile Leu Leu Val Leu Ser Tyr Val Ile
291          210          215
294 <210> SEQ ID NO: 5
295 <211> LENGTH: 377
296 <212> TYPE: PRT
297 <213> ORGANISM: Artificial Sequence
299 <220> FEATURE:
300 <223> OTHER INFORMATION: Description of Artificial Sequence:Pvs25-Pvs28
301     fusion protein
303 <400> SEQUENCE: 5
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305      1           5           10          15
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308          20          25          30
310 Glu Asn Thr Cys Glu Glu Lys Asn Glu Cys Lys Lys Glu Thr Leu Gly
311          35          40          45
313 Lys Ala Cys Gly Glu Phe Gly Gln Cys Ile Glu Asn Pro Asp Pro Ala
314          50          55          60
316 Gln Val Asn Met Tyr Lys Cys Gly Cys Ile Glu Gly Tyr Thr Leu Lys
317          65          70          75          80
319 Glu Asp Thr Cys Val Leu Asp Val Cys Gln Tyr Lys Asn Cys Gly Glu
320          85          90          95
322 Ser Gly Glu Cys Ile Val Glu Tyr Leu Ser Glu Ile Gln Ser Ala Gly
323          100         105         110
325 Cys Ser Cys Ala Ile Gly Lys Val Pro Asn Pro Glu Asp Glu Lys Lys
326          115         120         125
328 Cys Thr Lys Thr Gly Glu Thr Ala Cys Gln Leu Lys Cys Asn Thr Asp
329          130         135         140
331 Asn Glu Val Cys Lys Asn Val Glu Gly Val Tyr Lys Cys Gln Cys Met
332          145         150         155          160
334 Glu Gly Phe Thr Phe Asp Lys Glu Lys Asn Val Cys Leu Ser Gly Gly
335          165         170         175
337 Gly Pro Gly Gly Ala Lys Val Thr Ala Glu Thr Gln Cys Lys Asn
338          180         185         190
340 Gly Tyr Val Val Gln Met Ser Asn His Phe Glu Cys Lys Cys Asn Asp
341          195         200         205
343 Gly Phe Val Met Ala Asn Glu Asn Thr Cys Glu Glu Lys Arg Asp Cys
344          210         215         220

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**VERIFICATION SUMMARY**

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DATE: 06/30/2004

TIME: 13:03:06

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date